

p779.ST25
SEQUENCE LISTING

<110> Porro, Danilo

<120> Process for expression and secretion of proteins by the non-conventional yeast *Zygosaccharomyces bailii*

<130> p 779wo

<150> DE 10252245.6

<151> 2003-11-07

<160> 95

<170> PatentIn version 3.1

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35 40 45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
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<222> (1)..(75)

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Ser Tyr Phe Ser Leu Leu Val Ser Ala
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<222> (1)..(21)

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<213> Kluyver myces lactis

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Leu

<210> 37

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<213> *Saccharomyces cerevisiae*

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Phe Gly

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Thr Ser

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Leu Leu Ala Tyr Leu Val Leu Ser Leu Leu Phe Asn Ser Ala Leu Gly
 20 25 30

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<222> (1)..(21)

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<210> 61

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tacttaaadc attacgattc agagacttgc aaagatatca ttactcagta taatgttaac      360
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p779.ST25

Ile Tyr Thr Ser Ala Arg Asn Ile Leu Asp Arg Glu Tyr Thr Ala Asn
20 25 30

Glu Leu Lys Thr Ala Phe Gly Asp Glu Glu Ile Phe Thr Asp Leu Thr
35 40 45

Tyr His Ile His Val Asn Val Ser Gly Glu Ile Asp Ser Tyr Tyr His
50 55 60

Asn Leu Val Asn Phe Val Asp Asn Ala Leu Ala Asn Lys Asp Ile Asn
65 70 75 80

Arg Tyr Ile Tyr Ala Ile Phe Thr Gln Gln Thr Asn Tyr Thr Glu Asp
85 90 95

Gly Leu Ile Glu Tyr Leu Asn His Tyr Asp Ser Glu Thr Cys Lys Asp
100 105 110

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<213> Zygosaccharomyces bailii

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<213> *Zygosaccharomyces bailii*

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atctatccta tctga	435

<210> 65

<211> 299

<212> DNA

<213> *Zygosaccharomyces bailii*

<400> 65

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gagcttgacg gggaaagccg gcgaacgtgg cgagaaagga agggaagaaa gcgaaaggag	120
cgggcgctag ggcgctggca agtgtagcgg tcacgctgcg cgtaaccacc acacccgccg	180
cgcttaatgc gccgctacag ggcgcgtcag gtggcacttt tcgggggaaat gtgcgcggaa	240
cccctatttg tttatttttc taaatacatt caaatatgta tccgctcatg agacaataa	299

<210> 66

<211> 153

<212> DNA

<213> *Zygosaccharomyces bailii*

<400> 66

ctccactgta acatttccca ctgtcctttt cccatctttc attttacaat gagcaagttt	60
cagaaaaaaa aatacaaatg ggataagtgc aaaacattcc atgtatctgt agcttccaat	120
gttattcctc tctccagagt caggcttctg tgt	153

<210> 67

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<211> 231

<212> DNA

<213> Zygosaccharomyces bailii

<400> 67

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tctggagatt ttgcataaac aactgattta ttattagctt tattttctaa tccattaact	120
aattgatcat acataatata gatgaataag aataatgaaa ctagtgcaat aattgatcca	180
attgatgcta cataatttca accagcaaag gcatcagggt agtcaggaat t	231

<210> 68

<211> 52

<212> DNA

<213> Zygosaccharomyces bailii

<400> 68

ctcgtaaaaa cgagcatgag ctgcgtcagg tcagccgtgg atatcgttgc gg	52
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<210> 69

<211> 116

<212> DNA

<213> Zygosaccharomyces bailii

<400> 69

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<210> 70

<211> 268

<212> DNA

<213> Zygosaccharomyces bailii

<400> 70

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tgacgtaatc gatcgcggcg ccgagcccga tcgcctcgac gatcggcggc gtgccggcct	180
cgaacttgatg cggcggggtcg ccataggtga cccagtcctt ggcaacttca cggatcattt	240
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p779.ST25

<210> 71

<211> 869

<212> DNA

<213> *Zygosaccharomyces bailii*

<400> 71

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tgggtatgtc ccctgattcg acggcgtaaa ttgctggaat cttgtgttgg cgctaatagac    180
cgcttttttg aattatgtgc tatgcctctg ccattggtat caacagctga aatatttggt    240
gaagatcgaa tatcttctat tgtttctgag ggtatccccg aagctatggc gaaagaaagg    300
atctcttctc gtacttggat cggtagcaga agcaatagac gcacaatgca ttgacgcatac    360
ttgttgatac cgggtaatgt gagtcttctg ggttctgtta ttgagtttaa tatgtcgtcc    420
acctctgttc tcgtatccat tttgcgagta gcccgccata cagcacgtcc aatacaggag    480
aggccattta gcttcagggt cagagaagac acagcatggg gctcaccttc gagtgtctca    540
atagatgatt gagttgactg ggcttccgtg aaagggcctt tcgagagatc ttcagaaata    600
aaccagggtt gcgcttcatt agtaggtgtt cctggaggac tattgtcgct atctgctgga    660
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ataacattgc caaggccaat ttgaaagggt tcgcttatat gagtaaagag ctcggtgccc    780
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<210> 72

<211> 1425

<212> DNA

<213> *Zygosaccharomyces bailii*

<220>

<221> CDS

<222> (1)..(1425)

<223>

<400> 72

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1           5           10           15

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agg Arg	tta Leu	gct Ala 35	tct Ser	cta Leu	cta Leu	act Thr	atg Met 40	gtg Val	atc Ile	cta Leu	acg Thr	gtc Val 45	aac Asn	atg Met	tca Ser	144
aaa Lys	aag Lys 50	agg Arg	aag Lys	agc Ser	tct Ser	cca Pro 55	atc Ile	aag Lys	ctt Leu	agc Ser	acc Thr 60	ttt Phe	act Thr	aaa Lys	tat Tyr	192
cgt Arg 65	aga Arg	aat Asn	ggt Val	gcg Ala 70	aag Lys	tca Ser	ttg Leu	tat Tyr	tat Tyr	gat Asp 75	atg Met	tca Ser	agc Ser	aag Lys	aca Thr 80	240
gta Val	ttc Phe	ttc Phe	gaa Glu	tac Tyr 85	cat His	ctc Leu	aaa Lys	aat Asn	aca Thr 90	caa Gln	gat Asp	cta Leu	cag Gln	gag Glu 95	ggc Gly	288
ctc Leu	gag Glu	caa Gln	gcc Ala 100	att Ile	gcg Ala	ccc Pro	tac Tyr	aat Asn 105	ttc Phe	gtg Val	gta Val	aag Lys	gtg Val 110	cac His	aag Lys	336
aag Lys	cca Pro	att Ile 115	gat Asp	tgg Trp	cag Gln	aaa Lys	cag Gln	ctc Leu	tca Ser	agc Ser	gtg Val	cat His 125	gag Glu	agg Arg	aaa Lys	384
gcg Ala	ggc Gly 130	cac His	aga Arg	agc Ser	att Ile	ctc Leu 135	agc Ser	aac Asn	aat Asn	gtt Val	ggc Gly 140	gcc Ala	gag Glu	atc Ile	tct Ser	432
aaa Lys 145	ctg Leu	gct Ala	gag Glu	acg Thr	aaa Lys 150	gat Asp	tct Ser	act Thr	tgg Trp	agt Ser 155	ttt Phe	atc Ile	gag Glu	aga Arg	aca Thr 160	480
atg Met	gat Asp	ctg Leu	ata Ile	gaa Glu 165	gcc Ala	cgc Arg	acc Thr	cgc Arg	cag Gln 170	ccc Pro	acg Thr	aca Thr	aga Arg	gtt Val 175	gcg Ala	528
tat Tyr	agg Arg	ttt Phe	ctg Leu 180	ctt Leu	caa Gln	ctc Leu	aca Thr	ttc Phe 185	atg Met	aac Asn	tgc Cys	tgt Cys	agg Arg 190	gct Ala	aat Asn	576
gat Asp	ttg Leu	aaa Lys 195	aac Asn	gcc Ala	gac Asp	ccc Pro	agc Ser 200	act Thr	ttt Phe	caa Gln	atc Ile	atc Ile 205	gca Ala	gat Asp	cct Pro	624
cac His	ctt Leu 210	ggt Gly	cgt Arg	ata Ile	ttg Leu	cgg Arg 215	gcc Ala	ttt Phe	gtt Val	cca Pro	gag Glu 220	aca Thr	aag Lys	act Thr	agc Ser	672
att Ile 225	gaa Glu	agg Arg	ttt Phe	atc Ile	tat Tyr 230	ttt Phe	ttc Phe	cca Pro	tgt Cys	aag Lys 235	gga Gly	cga Arg	tgc Cys	gat Asp	ccg Pro 240	720
ctt Leu	ttg Leu	gct Ala	cta Leu	gat Asp 245	tcc Ser	tat Tyr	ctc Leu	ctg Leu	tgg Trp 250	gtt Val	ggc Gly	cca Pro	gtg Val	ccc Pro 255	aaa Lys	768
act Thr	cag Gln	act Thr	acc Thr 260	gat Asp	gaa Glu	gag Glu	act Thr	caa Gln 265	tat Tyr	gat Asp	tac Tyr	cag Gln	ctt Leu 270	ctt Leu	caa Gln	816
gat Asp	act Thr	ctc Leu 275	ttg Leu	att Ile	tcg Ser	tac Tyr	gac Asp 280	agg Arg	ttt Phe	atc Ile	gcc Ala	aaa Lys 285	gaa Glu	tca Ser	aag Lys	864

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gaa Glu 290	aat Asn 290	att Ile 290	ttc Phe 290	aaa Lys 290	ata Ile 290	cct Pro 295	aat Asn 295	ggg Gly 295	ccc Pro 295	aaa Lys 295	gct Ala 300	cat His 300	ttg Leu 300	ggg Gly 300	cgg Arg 300	912
cat His 305	cta Leu 305	atg Met 305	gca Ala 305	tca Ser 305	tac Tyr 310	ctt Leu 310	gga Gly 310	aac Asn 315	aac Asn 315	agt Ser 315	ctc Leu 315	aag Lys 315	agc Ser 315	gag Glu 320	gcc Ala 320	960
aca Thr 325	ctc Leu 325	tac Tyr 325	ggc Gly 325	aac Asn 325	tgg Trp 325	tct Ser 325	gtg Val 325	gaa Glu 330	agg Arg 330	caa Gln 330	gag Glu 335	ggc Gly 335	gtc Val 335	agc Ser 335	aaa Lys 335	1008
atg Met 340	gct Ala 340	gac Asp 340	agc Ser 340	cga Arg 340	tac Tyr 340	atg Met 345	cac His 345	acg Thr 345	gtt Val 345	aaa Lys 345	aaa Lys 345	agt Ser 350	cca Pro 350	cct Pro 350	tca Ser 350	1056
tat Tyr 355	cta Leu 355	ttt Phe 355	gca Ala 355	ttt Phe 355	tta Leu 355	tcc Ser 360	ggc Gly 360	tac Tyr 360	tac Tyr 360	aaa Lys 360	aag Lys 360	tcc Ser 365	aac Asn 365	caa Gln 365	ggc Gly 365	1104
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aca Thr 385	ctt Leu 385	cca Pro 385	ata Ile 385	aca Thr 390	acg Thr 390	aac Asn 390	gag Glu 390	aaa Lys 390	ttg Leu 395	atc Ile 395	tgt Cys 395	cgg Arg 395	cgg Arg 395	tac Tyr 400	ggg Gly 400	1200
aaa Lys 405	aat Asn 405	gcg Ala 405	aaa Lys 405	gtg Val 405	ata Ile 405	cca Pro 405	aaa Lys 405	gac Asp 410	gca Ala 410	ctg Leu 410	ctg Leu 410	tat Tyr 415	ctc Leu 415	tac Tyr 415	acg Thr 415	1248
tat Tyr 420	gcg Ala 420	cag Gln 420	cag Gln 420	aag Lys 420	cga Arg 420	aaa Lys 420	caa Gln 425	ttg Leu 425	gcc Ala 425	gat Asp 425	ccc Pro 430	aat Asn 430	gag Glu 430	caa Gln 430	aat Asn 430	1296
agg Arg 435	cta Leu 435	ttc Phe 435	agt Ser 435	agt Ser 435	gaa Glu 435	tca Ser 440	cca Pro 440	gcg Ala 440	cat His 440	ccc Pro 440	ttc Phe 445	tta Leu 445	act Thr 445	cct Pro 445	caa Gln 445	1344
tcg Ser 450	aca Thr 450	ggc Gly 450	tca Ser 450	tcg Ser 450	aca Thr 455	ccc Pro 455	ttg Leu 455	acc Thr 455	tggt Trp 455	act Thr 460	gct Ala 460	cca Pro 460	aag Lys 460	aca Thr 460	ctc Leu 460	1392
tcc Ser 465	act Thr 465	ggt Gly 465	cta Leu 465	atg Met 465	aca Thr 470	cct Pro 470	gga Gly 470	gaa Glu 470	gag Glu 470	tag Glu 470						1425

<210> 73

<211> 474

<212> PRT

<213> Zygosaccharomyces bailii

<400> 73

Met 1	Ser	Glu	Phe	Ser 5	Glu	Leu	Val	Arg	Ile 10	Leu	Pro	Leu	Asp	Gln 15	Val
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Ala	Glu	Ile	Lys 20	Arg	Ile	Leu	Ser	Arg 25	Gly	Asp	Pro	Ile	Pro 30	Leu	Gln
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p779.ST25

Arg Leu Ala Ser Leu Leu Thr Met Val Ile Leu Thr Val Asn Met Ser
 35 40 45

Lys Lys Arg Lys Ser Ser Pro Ile Lys Leu Ser Thr Phe Thr Lys Tyr
 50 55 60

Arg Arg Asn Val Ala Lys Ser Leu Tyr Tyr Asp Met Ser Ser Lys Thr
 65 70 75 80

Val Phe Phe Glu Tyr His Leu Lys Asn Thr Gln Asp Leu Gln Glu Gly
 85 90 95

Leu Glu Gln Ala Ile Ala Pro Tyr Asn Phe Val Val Lys Val His Lys
 100 105 110

Lys Pro Ile Asp Trp Gln Lys Gln Leu Ser Ser Val His Glu Arg Lys
 115 120 125

Ala Gly His Arg Ser Ile Leu Ser Asn Asn Val Gly Ala Glu Ile Ser
 130 135 140

Lys Leu Ala Glu Thr Lys Asp Ser Thr Trp Ser Phe Ile Glu Arg Thr
 145 150 155 160

Met Asp Leu Ile Glu Ala Arg Thr Arg Gln Pro Thr Thr Arg Val Ala
 165 170 175

Tyr Arg Phe Leu Leu Gln Leu Thr Phe Met Asn Cys Cys Arg Ala Asn
 180 185 190

Asp Leu Lys Asn Ala Asp Pro Ser Thr Phe Gln Ile Ile Ala Asp Pro
 195 200 205

His Leu Gly Arg Ile Leu Arg Ala Phe Val Pro Glu Thr Lys Thr Ser
 210 215 220

Ile Glu Arg Phe Ile Tyr Phe Phe Pro Cys Lys Gly Arg Cys Asp Pro
 225 230 235 240

Leu Leu Ala Leu Asp Ser Tyr Leu Leu Trp Val Gly Pro Val Pro Lys
 245 250 255

Thr Gln Thr Thr Asp Glu Glu Thr Gln Tyr Asp Tyr Gln Leu Leu Gln
 260 265 270

Asp Thr Leu Leu Ile Ser Tyr Asp Arg Phe Ile Ala Lys Glu Ser Lys
 275 280 285

Glu Asn Ile Phe Lys Ile Pro Asn Gly Pro Lys Ala His Leu Gly Arg
 290 295 300

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His Leu Met Ala Ser Tyr Leu Gly Asn Asn Ser Leu Lys Ser Glu Ala
 305 310 315 320

Thr Leu Tyr Gly Asn Trp Ser Val Glu Arg Gln Glu Gly Val Ser Lys
 325 330 335

Met Ala Asp Ser Arg Tyr Met His Thr Val Lys Lys Ser Pro Pro Ser
 340 345 350

Tyr Leu Phe Ala Phe Leu Ser Gly Tyr Tyr Lys Lys Ser Asn Gln Gly
 355 360 365

Glu Tyr Val Leu Ala Glu Thr Leu Tyr Asn Pro Leu Asp Tyr Asp Lys
 370 375 380

Thr Leu Pro Ile Thr Thr Asn Glu Lys Leu Ile Cys Arg Arg Tyr Gly
 385 390 395 400

Lys Asn Ala Lys Val Ile Pro Lys Asp Ala Leu Leu Tyr Leu Tyr Thr
 405 410 415

Tyr Ala Gln Gln Lys Arg Lys Gln Leu Ala Asp Pro Asn Glu Gln Asn
 420 425 430

Arg Leu Phe Ser Ser Glu Ser Pro Ala His Pro Phe Leu Thr Pro Gln
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Ser Thr Gly Leu Met Thr Pro Gly Glu Glu
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<210> 74

<211> 1074

<212> DNA

<213> *Zygosaccharomyces bailii*

<220>

<221> CDS

<222> (1)..(1074)

<223>

<400> 74

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ggt Val	cct Pro	tcc Ser 35	aag Lys	aat Asn	ata Ile	ctt Leu 40	atc Ile	aca Thr	cca Pro	aaa Lys	ggc Gly	aca Thr 45	ggt Val	gag Glu	ata Ile
cct Pro	gaa Glu 50	aac Asn	tat Tyr	caa Gln	aat Asn 55	tat Tyr 55	ccc Pro	ata Ile	ttg Leu	gcc Ala 60	atc Ile	ttc Phe	tac Tyr	gtc Val	aaa Lys
tat Tyr 65	tta Leu	atg Met	aag Lys	aaa Lys 70	aat Asn 70	ccg Pro	tac Tyr	gat Asp	ctt Leu 75	ctt Leu 75	cca Pro	agc Ser	acc Thr	gtg Val	aac Asn 80
tgg Trp	ccg Pro	gaa Glu	ccc Pro	tat Tyr 85	gta Val	gtg Val	gtg Val	aat Asn 90	acc Thr 90	atc Ile	act Thr	aag Lys	cgt Arg	ttc Phe 95	cag Gln
gac Asp	cat His	aaa Lys	cta Leu 100	ttt Phe	gca Ala	aac Asn	aaa Lys 105	aat Asn 105	gct Ala	gat Asp	gtc Val	tac Tyr 110	ggt Val	gaa Glu	aga Arg
ctt Leu	caa Gln 115	aat Asn 115	gca Ala	att Ile	gcc Ala	tcg Ser	ggt Gly 120	att Ile	aag Lys	att Ile	cct Pro	gag Glu 125	tct Ser	aag Lys	aag Lys
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att Ile 145	gag Glu	gag Glu	acc Thr	ttt Phe 150	att Ile 150	gat Asp	gcc Ala	act Thr	aat Asn 155	gcg Ala 155	aga Arg	aaa Lys	gaa Glu	ttg Leu	gat Asp 160
gag Glu	tac Tyr	ttc Phe	aga Arg	aaa Lys 165	ctt Leu 165	cag Gln	gat Asp	ggt Gly 170	aca Thr 170	tta Leu	acc Thr	gga Gly	gat Asp	ttg Leu 175	gag Glu
ggt Gly	ggc Gly	ttg Leu	tgc Cys 180	aag Lys	gtc Val	aaa Lys	acg Thr	ctc Leu 185	ata Ile	tcg Ser	tgt Cys	aaa Lys	gct Ala 190	ttg Leu	ttc Phe
gga Gly	gga Gly	cac His 195	acc Thr	caa Gln	gaa Glu	ctc Leu 200	cag Gln 200	ttt Phe	atg Met	gcc Ala	acc Thr	aat Asn 205	ggt Val	cgt Arg	aaa Lys
gtc Val	tgg Trp 210	ata Ile	ggg Gly	gag Glu	ata Ile	gtg Val 215	tgc Cys	ggc Gly	atg Met	gtt Val	tcc Ser 220	aat Asn	aaa Lys	aat Asn	gca Ala
att Ile 225	gac Asp	gat Asp	aat Asn	gat Asp	ctc Leu 230	gag Glu	gaa Glu	gaa Glu	gag Glu	cgt Arg 235	aat Asn	gca Ala	tcg Ser	ggc Gly	gaa Glu 240
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aat Asn	ggt Gly	ttg Leu	gac Asp 260	gct Ala	ctg Leu	aat Asn	act Thr	caa Gln 265	att Ile	aat Asn	gcc Ala	ata Ile	gaa Glu 270	acg Thr	gag Glu
gaa	tca	ttt	tgg	gaa	gct	atc	agg	gcg	ctc	cat	aat	gag	cta	cgc	acc

p779.ST25

Glu Ser Phe Trp Glu Ala Ile Arg Ala Leu His Asn Glu Leu Arg Thr
 275 280 285
 tct cca aca cag tta gaa gag tgc agg aaa gcg gca gtt ttt tta ctg 912
 Ser Pro Thr Gln Leu Glu Glu Cys Arg Lys Ala Ala Val Phe Leu Leu
 290 295 300
 ggc cat aaa aaa ata ctc caa aca ttt aca aag caa aag gat act gcc 960
 Gly His Lys Lys Ile Leu Gln Thr Phe Thr Lys Gln Lys Asp Thr Ala
 305 310 315 320
 cgc gct ctt ttt tat ata aat ctc aaa gag tgt ctg gga acc agc tgg 1008
 Arg Ala Leu Phe Tyr Ile Asn Leu Lys Glu Cys Leu Gly Thr Ser Trp
 325 330 335
 aat tta gaa tat aca gag gca tca gat gca aga aaa atg gca att aaa 1056
 Asn Leu Glu Tyr Thr Glu Ala Ser Asp Ala Arg Lys Met Ala Ile Lys
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 Gly Glu Leu Gln Asn
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<210> 75

<211> 357

<212> PRT

<213> Zygosaccharomyces bailii

<400> 75

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 35 40 45

Pro Glu Asn Tyr Gln Asn Tyr Pro Ile Leu Ala Ile Phe Tyr Val Lys
 50 55 60

Tyr Leu Met Lys Lys Asn Pro Tyr Asp Leu Leu Pro Ser Thr Val Asn
 65 70 75 80

Trp Pro Glu Pro Tyr Val Val Val Asn Thr Ile Thr Lys Arg Phe Gln
 85 90 95

Asp His Lys Leu Phe Ala Asn Lys Asn Ala Asp Val Tyr Val Glu Arg
 100 105 110

Leu Gln Asn Ala Ile Ala Ser Gly Ile Lys Ile Pro Glu Ser Lys Lys
 115 120 125

p779.ST25

Asn Glu Arg Leu Gly Gln Pro Lys Lys Thr Lys Asn Val Thr Lys Glu
 130 135 140

Ile Glu Glu Thr Phe Ile Asp Ala Thr Asn Ala Arg Lys Glu Leu Asp
 145 150 155 160

Glu Tyr Phe Arg Lys Leu Gln Asp Gly Thr Leu Thr Gly Asp Leu Glu
 165 170 175

Gly Gly Leu Cys Lys Val Lys Thr Leu Ile Ser Cys Lys Ala Leu Phe
 180 185 190

Gly Gly His Thr Gln Glu Leu Gln Phe Met Ala Thr Asn Val Arg Lys
 195 200 205

Val Trp Ile Gly Glu Ile Val Cys Gly Met Val Ser Asn Lys Asn Ala
 210 215 220

Ile Asp Asp Asn Asp Leu Glu Glu Glu Glu Arg Asn Ala Ser Gly Glu
 225 230 235 240

Gln Thr Thr Thr Ala Arg Glu Glu Ser Glu Ala Leu Asp Thr Thr Ser
 245 250 255

Asn Gly Leu Asp Ala Leu Asn Thr Gln Ile Asn Ala Ile Glu Thr Glu
 260 265 270

Glu Ser Phe Trp Glu Ala Ile Arg Ala Leu His Asn Glu Leu Arg Thr
 275 280 285

Ser Pro Thr Gln Leu Glu Glu Cys Arg Lys Ala Ala Val Phe Leu Leu
 290 295 300

Gly His Lys Lys Ile Leu Gln Thr Phe Thr Lys Gln Lys Asp Thr Ala
 305 310 315 320

Arg Ala Leu Phe Tyr Ile Asn Leu Lys Glu Cys Leu Gly Thr Ser Trp
 325 330 335

Asn Leu Glu Tyr Thr Glu Ala Ser Asp Ala Arg Lys Met Ala Ile Lys
 340 345 350

Gly Glu Leu Gln Asn
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<210> 76

<211> 750

<212> DNA

<213> Zygosaccharomyces bailii

p779.ST25

<220>

<221> CDS

<222> (1)..(750)

<223>

<400> 76

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gct ctc gat ctg ctt gaa cgg ctt gat tcc aac tgg aag ggc acc gag	96
Ala Leu Asp Leu Leu Glu Arg Leu Asp Ser Asn Trp Lys Gly Thr Glu	
20 25 30	
ctc ttt act cat ata cgc gaa acc ttt caa att ggc ctt ggc aat gtt	144
Leu Phe Thr His Ile Arg Glu Thr Phe Gln Ile Gly Leu Gly Asn Val	
35 40 45	
atc ata gtg tca gaa cag agt gaa agc ctt aga ata ccc cct tca cta	192
Ile Ile Val Ser Glu Gln Ser Glu Ser Leu Arg Ile Pro Pro Ser Leu	
50 55 60	
ctt ggt agc agt agt cca gca gat agc gac aat agt cct cca gga aca	240
Leu Gly Ser Ser Ser Pro Ala Asp Ser Asp Asn Ser Pro Pro Gly Thr	
65 70 75 80	
cct act aat gaa gcg caa ccc tgg ttt att tct gaa gat ctc tcg aaa	288
Pro Thr Asn Glu Ala Gln Pro Trp Phe Ile Ser Glu Asp Leu Ser Lys	
85 90 95	
ggc cct ttc acg gaa gcc cag tca act caa tca tct att gag aca ctc	336
Gly Pro Phe Thr Glu Ala Gln Ser Thr Gln Ser Ser Ile Glu Thr Leu	
100 105 110	
gaa ggt gag cac cat gct gtg tct tct ctg cac ctg aag cta aat ggc	384
Glu Gly Glu His His Ala Val Ser Ser Leu His Leu Lys Leu Asn Gly	
115 120 125	
ctc tcc tgt att gga cgt gct gta tgg cgg gct act cgc aaa atg gat	432
Leu Ser Cys Ile Gly Arg Ala Val Trp Arg Ala Thr Arg Lys Met Asp	
130 135 140	
acg aga aca gag gtg gac gac ata tta aac tca ata aca gaa ccc aga	480
Thr Arg Thr Glu Val Asp Asp Ile Leu Asn Ser Ile Thr Glu Pro Arg	
145 150 155 160	
aga ctc aca tta ccc ggt atc aac aag atg cgt caa tgc att gtg cgt	528
Arg Leu Thr Leu Pro Gly Ile Asn Lys Met Arg Gln Cys Ile Val Arg	
165 170 175	
cta ttg ctt ctc gta ccg atc caa gta cga gaa gag atc ctt tct ttc	576
Leu Leu Leu Leu Val Pro Ile Gln Val Arg Glu Glu Ile Leu Ser Phe	
180 185 190	
gcc ata gct tcg ggg ata ccc tca gaa aca ata gaa gat att cga tct	624
Ala Ile Ala Ser Gly Ile Pro Ser Glu Thr Ile Glu Asp Ile Arg Ser	
195 200 205	
tca aca aat att tca gct gtt gat acc aat ggc aga ggc ata gca cat	672
Ser Thr Asn Ile Ser Ala Val Asp Thr Asn Gly Arg Gly Ile Ala His	
210 215 220	

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aat tcc aaa aag cgg tca tta gcg cca aca caa gat tca cgc aat tta 720
 Asn Ser Lys Lys Arg Ser Leu Ala Pro Thr Gln Asp Ser Arg Asn Leu
 225 230 235 240

cgc cgt cga atc agg gga cat acc caa tag 750
 Arg Arg Arg Ile Arg Gly His Thr Gln
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<213> Zygosaccharomyces bailii

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Ala Leu Asp Leu Leu Glu Arg Leu Asp Ser Asn Trp Lys Gly Thr Glu
 20 25 30

Leu Phe Thr His Ile Arg Glu Thr Phe Gln Ile Gly Leu Gly Asn Val
 35 40 45

Ile Ile Val Ser Glu Gln Ser Glu Ser Leu Arg Ile Pro Pro Ser Leu
 50 55 60

Leu Gly Ser Ser Ser Pro Ala Asp Ser Asp Asn Ser Pro Pro Gly Thr
 65 70 75 80

Pro Thr Asn Glu Ala Gln Pro Trp Phe Ile Ser Glu Asp Leu Ser Lys
 85 90 95

Gly Pro Phe Thr Glu Ala Gln Ser Thr Gln Ser Ser Ile Glu Thr Leu
 100 105 110

Glu Gly Glu His His Ala Val Ser Ser Leu His Leu Lys Leu Asn Gly
 115 120 125

Leu Ser Cys Ile Gly Arg Ala Val Trp Arg Ala Thr Arg Lys Met Asp
 130 135 140

Thr Arg Thr Glu Val Asp Asp Ile Leu Asn Ser Ile Thr Glu Pro Arg
 145 150 155 160

Arg Leu Thr Leu Pro Gly Ile Asn Lys Met Arg Gln Cys Ile Val Arg
 165 170 175

Leu Leu Leu Leu Val Pro Ile Gln Val Arg Glu Glu Ile Leu Ser Phe
 180 185 190

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Ala Ile Ala Ser Gly Ile Pro Ser Glu Thr Ile Glu Asp Ile Arg Ser
 195 200 205

Ser Thr Asn Ile Ser Ala Val Asp Thr Asn Gly Arg Gly Ile Ala His
 210 215 220

Asn Ser Lys Lys Arg Ser Leu Ala Pro Thr Gln Asp Ser Arg Asn Leu
 225 230 235 240

Arg Arg Arg Ile Arg Gly His Thr Gln
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<210> 78

<211> 453

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 tctctcggat accacctcgg ttgaaactga caggtgggtt gttacgcatg ctaatgcaaa 240
 ggagcctata taccttttggc tcggctgctg taacagggaa tataaagggc agcataattt 300
 aggagtttag tgaacttgca acatttacta tttcccttc ttacgtaaat atttttcttt 360
 ttaattctaa atcaatcttt ttcaattttt tgtttgatt cttttcttgc ttaaattctat 420
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p779.ST25

<211> 499

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<222> (497)..(499)

<223> start codon

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cgtgtatcca tttgatactg tgctgggttac aagacacatg ctttacaagc acacttctat	180
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gtgcgtatgc gctgttaaca tatataaagg tcacctttcc ctgctcaaaa gagtcttagc	420
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32

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<211> 29

<212> DNA

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29

<210> 83

<211> 29

<212> DNA

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<220>

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<400> 84

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27

p779.ST25

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25

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25

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26

<210> 90

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<220>

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<212> DNA

<213> Zygosaccharomyces rouxii

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tcatacaact gtcctcctct tccgctctcg ccactagccg ccgaaccatt gctaccgcaa 420
tgacaccgtg tggatgatctc aaggaggat gtgtgggtgt gggacggaac ttccactttt 480
tcctcagtag gtgcgatgcc ccctacaccg agcttccact aacgtgtttc agcggttgaa 540
ggcaatggga tcgcagaatt atcgcagctt gttggtatat aaaggagaa gatatatgga 600
taagagacat gttctacttc tgttctctct ttctttttat cctatatcac cagaacaaat 660
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<210> 94

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29

<210> 95

<211> 25

<212> DNA

<213> artificial sequence

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<223> PCR primer

<400> 95

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25